### RAW SEQUENCE LISTING PATENT APPLICATION US/09/236,468

DATE: 02/10/1999 TIME: 16:12:12

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This Raw Listing contains the General Information Section and up to the first 5 pages.

1	SEQUENCE LISTING
2	SEQUENCE LISTING ENTERED
3	(1) General Information:
4	
5	(i) APPLICANT: Soppet, Daniel R
6	Yi, Li
7	Rosen, Craig A
8 9	Ruben, Steven
10	(ii) TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
11	HLTDG74
12	
13	(iii) NUMBER OF SEQUENCES: 8
14	\\( \)
15	(iv) CORRESPONDENCE ADDRESS:
16	(A) ADDRESSEE: Human Genome Sciences, Inc.
17	(B) STREET: 9410 Key West Ave
18	(C) CITY: Rockville
19	(D) STATE: MD
20	(E) COUNTRY: USA
21	(F) ZIP: 20850
22	/ )
23	(v) COMPUTER READABLE FORM:
24 25	(A) MEDIUM TYPE: Floppy disk
25 26	(B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27	(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28	(b) bollward. lacelelli kelease #1.0, velsion #1.50
29	(vi) CURRENT APPLICATION DATA:
30	(A) APPLICATION NUMBER:
31	(B) FILING DATE:
32	(C) CLASSIFICATION:
33	
34	(vi) PRIOR APPLICATION DATA:
35	(A) APPLICATION NUMBER: 08/468,011
36	(B) FILING DATE: 06-JUN-1995
37	(C) CLASSIFICATION:
38	/
39	(viii) ATTORNEY/AGENT INFORMATION:
40 41	(A) NAME: A. Anders Brookes (B) REGISTRATION NUMBER: 36,373
42	(C) REFERENCE/DOCKET NUMBER: PF201D1
43	(C) REPERENCE/DOCKET NORDER: FF201D1
44	(ix) TELECOMMUNICATION INFORMATION:
45	(A) TELEPHONE: 201-994-1700
46	(B) TELEFAX: 201-994-1744
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## RAW SEQUENCE LISTING PATENT APPLICATION US/09/236,468

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62	(A) NAME/KEY: CDS (B) LOCATION: 901712																
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73	CAC	GTC	TGG	GGT	TGG	CTA	ATG	CTC	GGC	AGC	TGC	CTC	CTG	GCC	AGA	GCC	161
74	His	Val	$\mathtt{Trp}$	Gly	Trp	Leu	Met	Leu	Gly	Ser	Cys	Leu	Leu	Ala	Arg	Ala	
75		10					15					20					
76																	
77	CAG	CTG	GAT	TCT	GAT	GGC	ACC	ATC	ACT	ATA	GAG	GAG	CAG	ATT	GTC	CTT	209
78	Gln	Leu	Asp	Ser	Asp	Gly	Thr	Ile	Thr	Ile	Glu	Glu	Gln	Ile	Val	Leu	
79	25					30					35					40	
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81	GTG	CTG	AAA	GCG	AAA	GTA	CAA	TGT	GAA	CTC	AAC	ATC	ACA	GCT	CAA	CTC	257
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85	CAG	GAG	GGA	GAA	GGT	AAT	TGT	TTC	CCT	GAA	TGG	GAT	GGA	CTC	ATT	TGT	305
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97															TGG		449
98		Asn	Gly	Inr	Trp	_	Pne	Met	His	ser		Asn	гåг	Thr	Trp		
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135	101	AAT	TAT	TCA	GAC	TGC	CTT	CGC	TTT	CTG	CAG	CCA	GAT	ATC	AGC	ATA	GGA	497
104	102	Asn	Tyr	Ser	Asp	Cys	Leu	Arg	Phe	Leu	Gln	Pro	Asp	Ile	Ser	Ile	Gly	
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TTC AGA CGA TTG CAT TGC ACT AGG AAC TAT ATC CAC ATG CAC TTA TTT  114 Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe 115 170 175 180 180  116 177 GTG TCT TTC ATG CTG AGA GCT ACA AGC ATC TTT GTC AAA GAC AGA GTA 118 Val Ser Phe Met Leu Arg Ala Thr Ser Ile Phe Val Lys Asp Arg Val 119 185 200  120 GTC CAT GCT CAC ATA GGA GTA AAG GAG CTG GAG TCC CTA ATA ATG CAG 121 Val His Ala His Ile Gly Val Lys Glu Leu Glu Ser Leu Ile Met Gln 122 Val His Ala His Ile Gly Val Lys Glu Leu Glu Ser Leu Ile Met Gln 123 205  124 215  125 GAT GAC CCA CAA AAT TCC ATT GAG GCA ACT TCT GTG GAC AAA TCA CAA 126 Asp Asp Pro Gln Asn Ser Ile Glu Ala Thr Ser Val Asp Lys Ser Gln 127 220  128 220  129 TAT ATC GGG TGC AAG ATT GCT GTG GTG ATG TTT ATT TAC TC CTG GCT 130 Tyr Ile Gly Cys Lys Ile Ala Val Val Met Phe Ile Tyr Phe Leu Ala 131 235  132 240  133 ACA AAT TAT TAT TGG ATC CTG GTG GAA GGT CTC TAC CTG CAT AAT CTC 134 Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Asn Leu 135 250  136  137 ATC TTT GTG GCT TTC TTT TCG GAC ACC AAA TAC CTG TGG GCT TTC LY Leu His Asn Leu 139 265  270 275  280  140  141 TTG ATA GGC TGG GGG TTT CCA GCA GCA ACT TTT GTT GCA GCA TGG GCT TGC 142 Leu Ile Gly Trp Gly Phe Pro Ala Ala Phe Val Ala Ala Trp Ala Val 141 TTG ATA GGC TGG GGT TTC CAG GCA GCA TTT GTT GCA GCA GCA TGG GCT GTG 142 Leu Ile Gly Trp Gly Phe Pro Ala Ala Phe Val Ala Ala Trp Ala Val 141 TTG ATA GGC TGG GGT GTT CCA GCA GCA TTT GTT GCA GCA GCA TGG GCT GTG 142 Leu Ile Gly Trp Gly Phe Pro Ala Ala Phe Val Ala Ala Trp Ala Val 143 285  144 290  150 Asp Ile Lys Trp Ile Tyr Gln Ala Pro Ile Leu Ala Ala Ile Gly Leu 151 310  152 Tyr Ile Gly Cry Trp Ile Leu Ala Arg Cys Trp Glu Leu Ser Ala Gly 147 300  150 Asp Ile Lys Trp Ile Tyr Gln Ala Pro Ile Leu Ala Ala Ile Gly Leu 151 315		261	116		FIIC	GLY	Ber	пец		vai	AIG	110	БСС			Gry	- 7 -	
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120	118	Val	Ser	Phe	Met	Leu	_	Ala	Thr	Ser	Ile		Val	Lys	Asp	Arg		
121   GTC CAT GCT CAC ATA GGA GTA AAG GAG GTA AAG GAG GAG CTG GAG TCC CTA ATA ATG CAG   737     122	119	185					190					195					200	
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124	122	Val	His	Ala	His	Ile	Gly	Val	Lys	Glu	Leu	Glu	Ser	Leu	Ile	Met	Gln	
125   GAT GAC   CCA   CAA   AAT   TCC   ATT   GAG   GCA   ACT   TCT   GTG   GAC   AAA   TCA   CAA   Asp   Asp   Asp   Asp   Pro   Gln   Asn   Ser   Ile   Glu   Ala   Thr   Ser   Val   Asp   Lys   Ser   Gln   230    128   129	123					205					210					215		
126       Asp Asp Pro Gln Asn Ser Ile Glu Ala Thr 225       Ser Val Asp Lys Ser Gln 230         127       220       225       230         128       TAT ATC GGG TGC AAG ATT GCT GTT GTG ATG TTT ATT TAC TTC CTG GCT 333       ATT TILE Gly Cys Lys Ile Ala Val Val Met Phe Ile Tyr Phe Leu Ala 245       245         130       Tyr Ile Gly Cys Lys Ile Ala Val Val Met Phe Ile Tyr Phe Leu Ala 245       245         131       235       CTG GTG GAA GGT CTC TAC CTG CAT AAT CTC 345         133       ACA AAT TAT TAT TAT TGG ATC CTG GTG GAA GGT CTC TAC CTG CAT AAT CTC 345         134       Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Asn Leu 255         135       250       255         136       250       255         137       ATC TTT GTG GCT TTC TTT TCG GAC ACC AAA TAC CTG TGG GGC TTC ATC 326       360         138       Ile Phe Val Ala Phe Phe Ser Asp Thr Lys Tyr Leu Trp Gly Phe Ile 327       280         140       TTG ATA GGC TGG GGG TTT CCA GCA GCA GCA TTT GTT GCA GCA TGG GCT GTG 327       360         141       TTG ATA GGC TGG GGG TTT CCA GCA GCA GCA TTT GTT GTT GTT GTT GTT GTT GTT GTT GT	124																	
127	125	GAT	GAC	CCA	CAA	AAT	TCC	ATT	GAG	GCA	ACT	TCT	GTG	GAC	AAA	TCA	CAA	785
128 129	126	Asp	Asp	Pro	Gln	Asn	Ser	Ile	Glu	Ala	Thr	Ser	Val	Asp	Lys	Ser	Gln	
TAT   ATC   GGG   TGC   AAG   ATT   GCT   GTT   GTG   ATG   TTT   ATT   TAC   TTC   CTG   GCT   GCT	127				220					225					230			
130	128																	
130	129	TAT	ATC	GGG	TGC	AAG	ATT	GCT	GTT	GTG	ATG	TTT	ATT	TAC	TTC	CTG	GCT	833
131	130																	
133       ACA AAT TAT TAT TAT TAT TGG ATC CTG GTG GAA GGT CTC TAC CTG CAT AAT CTC       881         134       Thr Asn Tyr Tyr Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Asn Leu       250         135       250       255       255       260         136       250       255       260       260         137       ATC TTT GTG GCT TTC TTT TCG GAC ACC AAA TAC CTG TGG GGC TTC ATC       929         138       Ile Phe Val Ala Phe Phe Ser Asp Thr Lys Tyr Leu Trp Gly Phe Ile       280         140       275       280         141       TTG ATA GGC TGG GGG TTT CCA GCA GCA TTT GTT GTT GCA GCA GCA TGG GCT GTG       977         142       Leu Ile Gly Trp Gly Phe Pro Ala Ala Phe Val Ala Ala Trp Ala Val       295         144       285       290       295         144       285       290       295         144       285       305       305         146       Ala Arg Ala Thr Leu Ala Asp Ala Arg Cys Trp Glu Leu Ser Ala Gly       310         147       300       305       310         148       349       GAC ATC AAG TGG ATT TAT CAA GCA CCG ATC TTA GCA GCT ATT GGG CTG       1073         150       Asp Ile Lys Trp Ile Tyr Gln Ala Pro Ile Leu Ala Ala Ala Ile Gly Leu       325	131	-		-	-	-								_				
134 Thr Asn Tyr Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Asn Leu 135	132																	
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135																		
136 137 ATC TTT GTG GCT TTC TTT TCG GAC ACC AAA TAC CTG TGG GGC TTC ATC 929 138 Ile Phe Val Ala Phe Phe Ser Asp Thr Lys Tyr Leu Trp Gly Phe Ile 139 265				-1-	-1-	F					1		_					
137       ATC TTT GTG GCT TTC TTT TCG GAC ACC AAA TAC CTG TGG GGC TTC ATC       929         138       Ile Phe Val Ala Phe Phe Ser Asp Thr Lys Tyr Leu Trp Gly Phe Ile       270       275       280         140       270       275       275       280       280         141       TTG ATA GGC TGG GGG TTT CCA GCA GCA TTT GTT GTT GCA GCA TGG GCT GTG GTG       977         142       Leu Ile Gly Trp Gly Phe Pro Ala Ala Phe Val Ala Ala Trp Ala Val 295       295         144       285       290       295         144       300       285       290       295         146       Ala Arg Ala Thr Leu Ala Asp Ala Arg Cys Trp Glu Leu Ser Ala Gly 310       1025         147       300       305       310         148       GAC ATC AAG TGG ATT TAT CAA GCA CCG ATC TTA GCA GCT ATT GGG CTG 1073         150       Asp Ile Lys Trp Ile Tyr Gln Ala Pro Ile Leu Ala Ala Ile Gly Leu 315       320																		
138		ATC	ттт	GTG	GCT	TTC	ттт	TCG	GAC	ACC	AAA	TAC	CTG	TGG	GGC	TTC	ATC	929
139																		3-2
140         141       TTG ATA GGC TGG GGG TTT CCA GCA GCA TTT GTT GCA GCA TGG GCT GTG       977         142       Leu Ile Gly Trp Gly Phe Pro Ala Ala Phe Val Ala Ala Trp Ala Val       285       290       295         144       GCA CGA GCA ACT CTG GCT GAT GCG AGG TGC TGG GAA CTT AGT GCT GGA       1025         146       Ala Arg Ala Thr Leu Ala Asp Ala Arg Cys Trp Glu Leu Ser Ala Gly       300       305       310         148       GAC ATC AAG TGG ATT TAT CAA GCA CCG ATC TTA GCA GCT ATT GGG CTG       1073         150       Asp Ile Lys Trp Ile Tyr Gln Ala Pro Ile Leu Ala Ala Ile Gly Leu       325								202			-7-	-			<b>0</b> -1			
141 TTG ATA GGC TGG GGG TTT CCA GCA GCA TTT GTT GCA GCA TGG GCT GTG 977  142 Leu Ile Gly Trp Gly Phe Pro Ala Ala Phe Val Ala Ala Trp Ala Val  143 285 290 295  144  145 GCA CGA GCA ACT CTG GCT GAT GCG AGG TGC TGG GAA CTT AGT GCT GGA  146 Ala Arg Ala Thr Leu Ala Asp Ala Arg Cys Trp Glu Leu Ser Ala Gly  147 300 305 305 310  148  149 GAC ATC AAG TGG ATT TAT CAA GCA CCG ATC TTA GCA GCT ATT GGG CTG  150 Asp Ile Lys Trp Ile Tyr Gln Ala Pro Ile Leu Ala Ala Ile Gly Leu  151 320 325		200					2,0											
142       Leu Ile Gly Trp Gly Phe Pro Ala Ala Phe Val Ala Ala Trp Ala Val         143       285       290       295         144         145       GCA CGA GCA ACT CTG GCT GAT GCG AGG TGC TGG GAA CTT AGT GCT GGA       1025         146       Ala Arg Ala Thr Leu Ala Asp Ala Arg Cys Trp Glu Leu Ser Ala Gly       300       305       305       310         148       GAC ATC AAG TGG ATT TAT CAA GCA CCG ATC TTA GCA GCT ATT GGG CTG       1073         150       Asp Ile Lys Trp Ile Tyr Gln Ala Pro Ile Leu Ala Ala Ile Gly Leu       325       325		ידידיכי	מידית	CCC	тсс	GGG	արար	CCA	CCA	GCA	սիսիսի	CTT	GCA	GCA	TGG	CCT	GTG	977
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153	AAT	TTT	ATT	CTG	TTT	CTG	AAT	ACG	GTT	AGA	GTT	CTA	GCT	ACC	AAA	ATC	1121
154	Asn	Phe	Ile	Leu	Phe	Leu	Asn	Thr	Val	Arg	Val	Leu	Ala	Thr	Lys	Ile	
155		330					335					340					
156																	
157												AAG					1169
158	$\mathtt{Trp}$	Glu	Thr	Asn	Ala		Gly	His	Asp	Thr	Arg	Lys	Gln	Tyr	Arg	Lys	
159	345					350					355					360	
160																	
161												TTT					1217
162	Leu	Ala	Lys	Ser	Thr	Leu	Val	Leu	Val	Leu	Val	Phe	Gly	Val	His	Tyr	
163					365					370					375		
164																	
165												GGG					1265
166	Ile	Val	Phe	Val	Cys	Leu	Pro	His	Ser	Phe	Thr	Gly	Leu	Gly	Trp	Glu	
167				380					385					390			
168																	
169												TTT					1313
170	Ile	Arg		His	Cys	Glu	Leu		Phe	Asn	Ser	Phe		Gly	Phe	Phe	
171			395					400					405				
172																	
173												GTT					1361
174	Val		Ile	Ile	Tyr	Cys	-	Cys	Asn	GLY	Glu	Val	Gln	Ala	Glu	Val	
175		410					415					420					
176					_												
177												GAC					1409
178	-	Lys	Met	Trp	Ser	_	Trp	Asn	Leu	Ser		Asp	Trp	Lys	Arg		
179	425					430					435					440	
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181												CTC					1457
182	Pro	Pro	Cys	GIY		Arg	Arg	Cys	GIY		vaı	Leu	Thr	Thr		Thr	
183					445					450					455		
184	~~~	3.00	3.00	3.00	300	~~~	maa.	<b>a</b> 3.a	ama	~~~	aa.	003	~~~	<b>a</b> a3	maa	maa	7505
185												GCA					1505
186	HIS	ser	Thr		ser	GIN	ser	GIII		Ala	Ala	Ala	HIS		ттр	Cys	
187				460					465					470			
188 189	TTT A	TI CITE	CITIC	CCA	7 7 C	CTTC	CCA	707	TICC	CCA	CCA	GAC	700	CTIC	7 (7 7	ccc	1553
190												Asp					1333
191	цец	ser	475	нта	цуъ	пеп	PLO	480	ser	PIO	Ата	ASP	485	пеп	1111	AIA	
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193	ልሮል	ጥሮል	СФФ	ሞልሮ	СТС	ССТ	ልጥር	тСт	CCA	СΤΆ	ΣСΤ	CAG	AGC	A CC	ΔСΤ	GCC	1601
194												Gln					1001
195	1111	490	Deu	171	Deu	ALG	495	001	O-y	Val	1111	500	DCI	n-9	1111	ALG	
196		470					173					500					
197	тса	CAC	АСТ	כייכ	דככ	ACC	AGG	AGC	AAC	AAG	GAA	GAT	АСТ	GGG	AGG	CAG	1649
198												Asp					1049
199	505	****		u	JUL	510	9	JC1		_y 5	515	P		y	9	520	
200	505															220	
201	AGA	GAT	GAT	Αππ	СТА	АТС	GAG	AAG	ССТ	TCC	AGG	CCT	ATG	GAA	тст	AAC	1697
202												Pro					1057
202	3	٠٢			525			-15		530	5				535		
204																	
205	CCA	GAC	ACT	GAA	GGA	TGAG	CAAGO	GAG A	AAACI	rgago	A TO	GTTC:	CTG	ATC	GAC	ATGT	1752
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## RAW SEQUENCE LISTING PATENT APPLICATION US/09/236,468

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														IN	PUI	3E1: 3303	ss.raw
206	Pro	Asp	Thr	Glu	Gly												
207				540													
208																	
209	GTGG	CTG	ACT 1	TTCAT	rggg	CT GO	FTCC	AATG	G CTC	GTTC	STGT	GAG	AGGG	CTT (	GCTC	SATACT	1812
210																	
211	CCTATGCTTG AGCACAAAGG CTGAAAATTC AGTTAAGGTG TTACTTAATA ATAGTTTTTA 187															1872	
212	GGCTCCATGA ATTGGCTCCT GTAAATACTA ACGACATGAA AATGCAAGTG TCAATGGAGT 193																
213	GGCT	CCAT	rga A	ATTGO	CTC	CT GT	CAAA?	ract?	A ACC	GACAT	rgaa	AATO	CAA	TG :	rcaa:	rggagt	1932
214																	
215	AGTT	TATI	CAC (	CTTCT	CATTO	G CA	ATCA	AGTT:	r TC	CTCTA	TAAP	TAAT	GTA:	rgg :	TTTAT	<b>FGCTCT</b>	1992
216																	
217	GTGA	TTGT	TC A	Ą													2003
218																	
219																	
220	(2) INFORMATION FOR SEQ ID NO:2:																
221	• •					~											
222	(i) SEQUENCE CHARACTERISTICS:																
223	(A) LENGTH: 541 amino acids																
224	(B) TYPE: amino acid																
225	(D) TOPOLOGY: linear																
226	(D) IOPOLOGI: IIIIeal																
227	(ii) MOLECULE TYPE: protein																
228	(11) MOLECULE TYPE: protein																
229	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:																
230		(1	· - / ·	2201	J1101					2							
231	Met	Δla	Trn	T.e11	Glv	Δla	Ser	T.@11	His	Val	Trn	Glv	Trn	Len	Met	Leu	
232	1	лια	110	шси	5	mu	501	LCu		10		017			15	200	
233	_																
234	Glaz	gar	Cve	T.011	T.011	Δla	Δνα	Δla	Gln	T.e.11	Δen	Ser	Δsn	Glv	Thr	Tle	
235	GIY	Ser	Cys	20	пси	ALG	n. g	AIG	25	11Cu	пор		пор	30		110	
236				20					23					50			
237	Thr	Tla	Clu	Glu	Gln	Tla	77 a 7	T.011	v-1	T.011	Tare	Λla	Lare	172 l	Gln	Cve	
238	1111	TTC	35	GIU	GIII	116	vai	40	val	пец	БУЗ	AIG	45	Val	GIII	Cys	
239			33					40					43				
240	<b>a</b> 1	T 01/	7	т1.	mb.~	7 J -	<i>~</i> 1~	T 011	C15	C1	C1	C1.,	C1.,	7 cn	Cys	Pho	•
241	GIU	50	ASII	116	1111	мта	55	пеп	GIII	GIU	GIY	60	GIY	veii	Cys	FIIC	
241		50					33					00					
	Dwo	a1	M	7 ~~	<b>~1</b>	T 011	т10	Crra	П	Dro	7 ~~	C1	Thr	170 T	C111	Two	
243	65	GIU	Trp	Asp	GIY	70	TIE	Cys	пр	PIO	75	GIY	1111	vaı	Gly	80 80	
244	65					70					/5					80	
245	<b>T</b> 1-	a		77- 7	D	C	D===	Desc	TT	T1.	m	7 ~~	Dho	7 an	111.0	T ***	
246	тте	ser	Ala	vai		Cys	PIO	PIO	TYL		TYL	Asp	Pne	ASII	His	пув	
247					85					90					95		
248	<b>~</b> 1	**- 7		D1	3	77.2 m	G	3	D	3	<b>a</b> 3	mb		7	Dha	Mot	
249	GТĀ	val	Ala		arg	HIS	cys	ASI		ASN	GTA	ınr	rrb		Phe	Mec	
250				100					105					110			
251	***	<b>a</b> -	<b>.</b> .			m1	m	<b>77.</b>	<b>3</b>	m	<b>0</b>	3	<b>~</b>	T	7	Dh e	
252	Hls	ser		Asn	гла	Tnr	Trp		Asn	Tyr	ser	Asp		ьeu	Arg	rne	
253			115					120					125				
254	_		_	_		_		~-	_		~-	_,	_	<b>~</b> 3	_	•	
255			Pro	Asp	Ile	Ser		GLY	Lys	Gln	Glu		Cys	Glu	Arg	ьeu	
256		130					135					140					
257	_				_,			_	_			-1	~-	_	_		
258	Tyr	Val	Met	Tyr	Thr	Val	GLY	Tyr	Ser	Ile	ser	Phe	GIY	Ser	Leu	Ala	

# SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/09/236,468

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